SEQUENCE LISTING

<110> Bandaru, Rajasekhar

<120> 68730 and 69112, Protein Kinase
Molecules and Uses Therefor

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aag ctg cgc cgc agc ccg agc cgc ccg gca tcc ccg ccg cct ctg cgc   98
Lys Leu Arg Arg Ser Pro Ser Arg Pro Ala Ser Pro Pro Pro Leu Arg
 15                  20                  25                  30

ccg cgc cgc gcc ccc ggc gcc ccc tcc cca gcg cgc ccc cgg ccg ctc   146
Pro Arg Arg Ala Pro Gly Ala Pro Ser Pro Ala Arg Pro Arg Pro Leu
                 35                  40                  45

ctc cgc gcc gcg ctc gtc ggc cat ggc ccg gga gaa cgg cga gag cag   194
Leu Arg Ala Ala Leu Val Gly His Gly Pro Gly Glu Arg Arg Glu Gln
             50                  55                  60

ctc ctc ctg gaa aaa gca agc tga aga cat caa gaa gat ctt cga gtt   242
Leu Leu Leu Glu Lys Ala Ser  *  Arg His Gln Glu Asp Leu Arg Val
         65                      70                  75

caa aga gac cct cgg aac cgg ggc ctt ttc cga agt ggt ttt agc tga   290
Gln Arg Asp Pro Arg Asn Arg Gly Leu Phe Arg Ser Gly Phe Ser  *
         80                  85                  90
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aga gaa ggc aac tgg caa gct ctt tgc tgt gaa gtg tat ccc taa gaa   338
Arg Glu Gly Asn Trp Gln Ala Leu Cys Cys Glu Val Tyr Pro  *  Glu
         95                  100                 105

ggc gct gaa ggg caa gga aag cag cat aga gaa tga gat agc cgt cct   386
Gly Ala Glu Gly Gln Gly Lys Gln His Arg Glu  *  Asp Ser Arg Pro
        110                 115                 120

gag aaa gat taa gca tga aaa tat tgt tgc cct gga aga cat tta tga   434
Glu Lys Asp  *  Ala  *  Lys Tyr Cys Cys Pro Gly Arg His Leu  *
        125                 130                 135

aag ccc aaa tca cct gta ctt ggt cat gca gct ggt gtc cgg tgg aga   482
Lys Pro Lys Ser Pro Val Leu Gly His Ala Ala Gly Val Arg Trp Arg
                140                 145                 150

gct gtt tga ccg gat agt gga gaa ggg gtt tta tac aga gaa gga tgc   530
Ala Val  *  Pro Asp Ser Gly Glu Gly Val Leu Tyr Arg Glu Gly Cys
                155                 160                 165

cag cac tct gat ccg cca agt ctt gga cgc cgt gta cta tct cca cag   578
Gln His Ser Asp Pro Pro Ser Leu Gly Arg Arg Val Leu Ser Pro Gln
            170                 175                 180

aat ggg cat cgt cca cag aga cct caa gcc cga aaa tct ctt gta cta   626
Asn Gly His Arg Pro Gln Arg Pro Gln Ala Arg Lys Ser Leu Val Leu
        185                 190                 195

cag tca aga tga gga gtc caa aat aat gat cag tga ctt tgg att gtc   674
Gln Ser Arg  *  Gly Val Gln Asn Asn Asp Gln  *  Leu Trp Ile Val
    200                 205                 210

aaa aat gga ggg caa agg aga tgt gat gtc cac tgc ctg tgg aac tcc   722
Lys Asn Gly Gly Gln Arg Arg Cys Asp Val His Cys Leu Trp Asn Ser
        215                 220                 225

agg cta tgt cgc tcc tga agt cct cgc cca gaa acc tta cag caa agc   770
Arg Leu Cys Arg Ser  *  Ser Pro Arg Pro Glu Thr Leu Gln Gln Ser
    230                 235                 240

cgt tga ctg ctg gtc cat cgg agt gat tgc cta cat ctt gct ctg cgg   818
Arg  *  Leu Leu Val His Arg Ser Asp Cys Leu His Leu Ala Leu Arg
        245                 250                 255

cta ccc tcc ttt tta tga tga aaa tga ctc caa gct ctt tga gca gat   866
Leu Pro Ser Phe Leu  *   *  Lys  *  Leu Gln Ala Leu  *  Ala Asp
    260                             265                     270

cct caa ggc gga ata tga gtt tga ctc tcc cta ctg gga tga cat ctc   914
Pro Gln Gly Gly Ile  *  Val  *  Leu Ser Leu Leu Gly  *  His Leu
                275                         280

cga ctc tgc aaa aga ctt cat tcg gaa cct gat gga gaa gga ccc gaa   962
Arg Leu Cys Lys Arg Leu His Ser Glu Pro Asp Gly Glu Gly Pro Glu
    285                 290                 295
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taa aag ata cac gtg tga gca ggc agc tcg gca ccc atg gat cgc tgg   1010
 *  Lys Ile His Val  *  Ala Gly Ser Ser Ala Pro Met Asp Arg Trp
    300                     305                 310

tga cac agc cct caa caa aaa cat cca cga gtc cgt cag cgc cca gat   1058
 *  His Ser Pro Gln Gln Lys His Pro Arg Val Arg Gln Arg Pro Asp
        315                 320                 325

ccg gaa aaa ctt tgc caa gag caa atg gag aca agc att taa tgc cac   1106
Pro Glu Lys Leu Cys Gln Glu Gln Met Glu Thr Ser Ile  *  Cys His
    330                 335                 340

ggc cgt cgt gag aca tat gag aaa act aca cct cgg cag cag cct gga   1154
Gly Arg Arg Glu Thr Tyr Glu Lys Thr Thr Pro Arg Gln Gln Pro Gly
    345                 350                 355

cag ttc aaa tgc aag tgt ttc gag cag cct cag ttt ggc cag cca aaa   1202
Gln Phe Lys Cys Lys Cys Phe Glu Gln Pro Gln Phe Gly Gln Pro Lys
360                 365                 370                 375

aga ctg tgc gta tgt agc aaa acc aga atc cct cag ctg a cactgaagac  1252
Arg Leu Cys Val Cys Ser Lys Thr Arg Ile Pro Gln Leu
                380                 385

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Arg Ala Pro Gly Ala Pro Ser Pro Ala Arg Pro Arg Pro Leu Leu Arg
        35                  40                  45
Ala Ala Leu Val Gly His Gly Pro Gly Glu Arg Arg Glu Gln Leu Leu
    50                  55                  60
Leu Glu Lys Ala Ser Arg His Gln Glu Asp Leu Arg Val Gln Arg Asp
65                  70                  75                  80
Pro Arg Asn Arg Gly Leu Phe Arg Ser Gly Phe Ser Arg Glu Gly Asn
                85                  90                  95
Trp Gln Ala Leu Cys Cys Glu Val Tyr Pro Glu Gly Ala Glu Gly Gln
            100                 105                 110
Gly Lys Gln His Arg Glu Asp Ser Arg Pro Glu Lys Asp Ala Lys Tyr
        115                 120                 125
Cys Cys Pro Gly Arg His Leu Lys Pro Lys Ser Pro Val Leu Gly His
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    130                 135                 140
Ala Ala Gly Val Arg Trp Arg Ala Val Pro Asp Ser Gly Glu Gly Val
145                 150                 155                 160
Leu Tyr Arg Glu Gly Cys Gln His Ser Asp Pro Pro Ser Leu Gly Arg
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Arg Val Leu Ser Pro Gln Asn Gly His Arg Pro Gln Arg Pro Gln Ala
            180                 185                 190
Arg Lys Ser Leu Val Leu Gln Ser Arg Gly Val Gln Asn Asn Asp Gln
        195                 200                 205
Leu Trp Ile Val Lys Asn Gly Gly Gln Arg Arg Cys Asp Val His Cys
    210                 215                 220
Leu Trp Asn Ser Arg Leu Cys Arg Ser Ser Pro Arg Pro Glu Thr Leu
225                 230                 235                 240
Gln Gln Ser Arg Leu Leu Val His Arg Ser Asp Cys Leu His Leu Ala
                245                 250                 255
Leu Arg Leu Pro Ser Phe Leu Lys Leu Gln Ala Leu Ala Asp Pro Gln
            260                 265                 270
Gly Gly Ile Val Leu Ser Leu Leu Gly His Leu Arg Leu Cys Lys Arg
        275                 280                 285
Leu His Ser Glu Pro Asp Gly Glu Gly Pro Glu Lys Ile His Val Ala
    290                 295                 300
Gly Ser Ser Ala Pro Met Asp Arg Trp His Ser Pro Gln Gln Lys His
305                 310                 315                 320
Pro Arg Val Arg Gln Arg Pro Asp Pro Glu Lys Leu Cys Gln Glu Gln
                325                 330                 335
Met Glu Thr Ser Ile Cys His Gly Arg Arg Glu Thr Tyr Glu Lys Thr
            340                 345                 350
Thr Pro Arg Gln Gln Pro Gly Gln Phe Lys Cys Lys Cys Phe Glu Gln
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gaagagaagg caactggcaa gctctttgct gtgaagtgta tccctaagaa ggcgctgaag 180
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gagaaggacc cgaataaaag atacacgtgt gagcaggcag ctcggcaccc atggatcgct 840
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tttgccaaga gcaaatggag acaagcattt aatgccacgg ccgtcgtgag acatatgaga 960

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               1               5                  10

gct gta gaa gaa ctg tac ccc aac aaa gcc cgg gcc ctg aca ctg gcc   1299
Ala Val Glu Glu Leu Tyr Pro Asn Lys Ala Arg Ala Leu Thr Leu Ala
     15                  20                  25

cag cac agc cgt gcc cct tct cca agg ctg agg agc agg ctg ttt agc   1347
Gln His Ser Arg Ala Pro Ser Pro Arg Leu Arg Ser Arg Leu Phe Ser
 30                  35                  40                  45

aag gct ctg aaa gga gac cac cgc tgt ggg gag acc gag acc ccc aag   1395
Lys Ala Leu Lys Gly Asp His Arg Cys Gly Glu Thr Glu Thr Pro Lys
                 50                  55                  60

agc tgc agc gaa gtt gca gga tgc aag gca gcc atg agg cac cag ggg   1443
Ser Cys Ser Glu Val Ala Gly Cys Lys Ala Ala Met Arg His Gln Gly
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                65                  70                  75

aag atc ccc gag gag ctt tca cta gat gac aga gcg agg acc cag aag   1491
Lys Ile Pro Glu Glu Leu Ser Leu Asp Asp Arg Ala Arg Thr Gln Lys
         80                  85                  90

aag tgg ggg agg ggg aaa tgg gag cca gaa ccc agt agc aag ccc ccc   1539
Lys Trp Gly Arg Gly Lys Trp Glu Pro Glu Pro Ser Ser Lys Pro Pro
     95                 100                 105

agg gaa gcc act ctg gaa gag agg cac gca agg gga gag aag cat ctt   1587
Arg Glu Ala Thr Leu Glu Glu Arg His Ala Arg Gly Glu Lys His Leu
110                 115                 120                 125

ggg gtg gag att gaa aag acc tcg ggt gaa att atc aga tgc gag aag   1635
Gly Val Glu Ile Glu Lys Thr Ser Gly Glu Ile Ile Arg Cys Glu Lys
                130                 135                 140

tgc aag aga gag agg gag ctc cag cag agc ctg gag cgt gag agg ctt   1683
Cys Lys Arg Glu Arg Glu Leu Gln Gln Ser Leu Glu Arg Glu Arg Leu
            145                 150                 155

tct ctg ggg acc agt gag ctg gat atg ggg aag ggc cca atg tat gat   1731
Ser Leu Gly Thr Ser Glu Leu Asp Met Gly Lys Gly Pro Met Tyr Asp
        160                 165                 170

gtg gag aag ctg gtg agg acc aga agc tgc agg agg tct ccc gag gca   1779
Val Glu Lys Leu Val Arg Thr Arg Ser Cys Arg Arg Ser Pro Glu Ala
    175                 180                 185

aat cct gca agt ggg gag gaa ggg tgg aag ggt gac agc cac agg agc   1827
Asn Pro Ala Ser Gly Glu Glu Gly Trp Lys Gly Asp Ser His Arg Ser
190                 195                 200                 205

agc ccc agg aat ccc act caa gag ctg agg aga ccc agc aag agc atg   1875
Ser Pro Arg Asn Pro Thr Gln Glu Leu Arg Arg Pro Ser Lys Ser Met
                210                 215                 220

gac aag aaa gag gac aga ggc cca gag gat caa gaa agc cat gct cag   1923
Asp Lys Lys Glu Asp Arg Gly Pro Glu Asp Gln Glu Ser His Ala Gln
            225                 230                 235

gga gca gcc aag gcc aag aag gac ctt gtg gaa gtt ctt cct gtc aca   1971
Gly Ala Ala Lys Ala Lys Lys Asp Leu Val Glu Val Leu Pro Val Thr
        240                 245                 250

gag gag ggg ctg agg gag gtg aag aag gac acc agg ccc atg agc agg   2019
Glu Glu Gly Leu Arg Glu Val Lys Lys Asp Thr Arg Pro Met Ser Arg
    255                 260                 265

agc aaa cat ggt ggc tgg ctc ctg aga gag cac cag gcg ggc ttt gag   2067
Ser Lys His Gly Gly Trp Leu Leu Arg Glu His Gln Ala Gly Phe Glu
270                 275                 280                 285

aag ctc cgc agg acc cga gga gaa gag aag gag gca gag aag gag aaa   2115
Lys Leu Arg Arg Thr Arg Gly Glu Glu Lys Glu Ala Glu Lys Glu Lys
                290                 295                 300
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aag cca tgt atg tct gga ggc aga agg atg act ctc aga gat gac caa   2163
Lys Pro Cys Met Ser Gly Gly Arg Arg Met Thr Leu Arg Asp Asp Gln
            305                 310                 315

cct gca aag cta gaa aag gag ccc aag acg agg cca gaa gag aac aag   2211
Pro Ala Lys Leu Glu Lys Glu Pro Lys Thr Arg Pro Glu Glu Asn Lys
        320                 325                 330

cca gag cgg ccc agc ggt cgg aag cca cgg ccc atg ggc atc att gcc   2259
Pro Glu Arg Pro Ser Gly Arg Lys Pro Arg Pro Met Gly Ile Ile Ala
    335                 340                 345

gcc aat gtg gaa aag cat tat gag act ggc cgg gtc att ggg gat ggg   2307
Ala Asn Val Glu Lys His Tyr Glu Thr Gly Arg Val Ile Gly Asp Gly
350                 355                 360                 365

aac ttt gct gtc gtg aag gag tgc aga cac cgc gag acc agg cag gcc   2355
Asn Phe Ala Val Val Lys Glu Cys Arg His Arg Glu Thr Arg Gln Ala
                370                 375                 380

tat gcg atg aag atc att gac aag tcc aga ctc aag ggc aag gag gac   2403
Tyr Ala Met Lys Ile Ile Asp Lys Ser Arg Leu Lys Gly Lys Glu Asp
            385                 390                 395

atg gtg gac agt gag atc ttg atc atc cag agc ctc tct cac ccc aac   2451
Met Val Asp Ser Glu Ile Leu Ile Ile Gln Ser Leu Ser His Pro Asn
        400                 405                 410

atc gtg aaa ttg cat gaa gtc tac gaa aca gac atg gaa atc tac ctg   2499
Ile Val Lys Leu His Glu Val Tyr Glu Thr Asp Met Glu Ile Tyr Leu
    415                 420                 425

atc ctg gag tac gtg cag gga gga gac ctt ttt gac gcc atc ata gaa   2547
Ile Leu Glu Tyr Val Gln Gly Gly Asp Leu Phe Asp Ala Ile Ile Glu
430                 435                 440                 445

agt gtg aag ttc ccg gag ccc gat gct gcc ctc atg atc atg gac tta   2595
Ser Val Lys Phe Pro Glu Pro Asp Ala Ala Leu Met Ile Met Asp Leu
                450                 455                 460

tgc aaa gcc ctc gtc cac atg cac gac aag agc att gtc cac cgg gac   2643
Cys Lys Ala Leu Val His Met His Asp Lys Ser Ile Val His Arg Asp
            465                 470                 475

ctc aag ccg gaa aac ctt ttg gtt cag cga aat gag gac aaa tct act   2691
Leu Lys Pro Glu Asn Leu Leu Val Gln Arg Asn Glu Asp Lys Ser Thr
        480                 485                 490

acc ttg aaa ttg gct gat ttt gga ctt gca aag cat gtg gtg aga cct   2739
Thr Leu Lys Leu Ala Asp Phe Gly Leu Ala Lys His Val Val Arg Pro
    495                 500                 505

ata ttt act gtg tgt ggg acc cca act tac gta gct ccc gaa att ctt   2787
Ile Phe Thr Val Cys Gly Thr Pro Thr Tyr Val Ala Pro Glu Ile Leu
510                 515                 520                 525
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Ser Glu Lys Gly Tyr Gly Leu Glu Val Asp Met Trp Ala Ala Gly Val
                530                 535                 540

atc ctc tat atc ctg ctg tgt ggc ttt ccc cca ttc cgc agc cct gag   2883
Ile Leu Tyr Ile Leu Leu Cys Gly Phe Pro Pro Phe Arg Ser Pro Glu
            545                 550                 555

agg gac cag gac gag ctc ttt aac atc atc cag ctg ggc cac ttt gag   2931
Arg Asp Gln Asp Glu Leu Phe Asn Ile Ile Gln Leu Gly His Phe Glu
        560                 565                 570

ttc ctc ccc cct tac tgg gac aat atc tct gat gct gct aaa gat ctg   2979
Phe Leu Pro Pro Tyr Trp Asp Asn Ile Ser Asp Ala Ala Lys Asp Leu
    575                 580                 585

gtg agc cgg ttg ctg gtg gta gac ccc aaa aag cgc tac aca gct cat   3027
Val Ser Arg Leu Leu Val Val Asp Pro Lys Lys Arg Tyr Thr Ala His
590                 595                 600                 605

cag gtt ctt cag cac ccc tgg atc gaa aca gct ggc aag acc aat aca   3075
Gln Val Leu Gln His Pro Trp Ile Glu Thr Ala Gly Lys Thr Asn Thr
                610                 615                 620

gtg aaa cga cag aag cag gtg tcc ccc agc agc gag ggt cac ttc cgg   3123
Val Lys Arg Gln Lys Gln Val Ser Pro Ser Ser Glu Gly His Phe Arg
            625                 630                 635

agc cag cac aag agg gtt gtg gag cag gta tca tag tcaccacctt        3169
Ser Gln His Lys Arg Val Val Glu Gln Val Ser  *
        640                 645

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            20                  25                  30
Arg Ala Pro Ser Pro Arg Leu Arg Ser Arg Leu Phe Ser Lys Ala Leu
        35                  40                  45
Lys Gly Asp His Arg Cys Gly Glu Thr Glu Thr Pro Lys Ser Cys Ser
    50                  55                  60
Glu Val Ala Gly Cys Lys Ala Ala Met Arg His Gln Gly Lys Ile Pro
65                  70                  75                  80
Glu Glu Leu Ser Leu Asp Asp Arg Ala Arg Thr Gln Lys Lys Trp Gly
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                    85                  90                  95
Arg Gly Lys Trp Glu Pro Glu Pro Ser Ser Lys Pro Pro Arg Glu Ala
                100                 105                 110
Thr Leu Glu Glu Arg His Ala Arg Gly Glu Lys His Leu Gly Val Glu
            115                 120                 125
Ile Glu Lys Thr Ser Gly Glu Ile Ile Arg Cys Glu Lys Cys Lys Arg
        130                 135                 140
Glu Arg Glu Leu Gln Gln Ser Leu Glu Arg Glu Arg Leu Ser Leu Gly
145                 150                 155                 160
Thr Ser Glu Leu Asp Met Gly Lys Gly Pro Met Tyr Asp Val Glu Lys
                165                 170                 175
Leu Val Arg Thr Arg Ser Cys Arg Arg Ser Pro Glu Ala Asn Pro Ala
            180                 185                 190
Ser Gly Glu Glu Gly Trp Lys Gly Asp Ser His Arg Ser Ser Pro Arg
        195                 200                 205
Asn Pro Thr Gln Glu Leu Arg Arg Pro Ser Lys Ser Met Asp Lys Lys
    210                 215                 220
Glu Asp Arg Gly Pro Glu Asp Gln Glu Ser His Ala Gln Gly Ala Ala
225                 230                 235                 240
Lys Ala Lys Lys Asp Leu Val Glu Val Leu Pro Val Thr Glu Glu Gly
                245                 250                 255
Leu Arg Glu Val Lys Lys Asp Thr Arg Pro Met Ser Arg Ser Lys His
            260                 265                 270
Gly Gly Trp Leu Leu Arg Glu His Gln Ala Gly Phe Glu Lys Leu Arg
        275                 280                 285
Arg Thr Arg Gly Glu Glu Lys Glu Ala Glu Lys Glu Lys Lys Pro Cys
    290                 295                 300
Met Ser Gly Gly Arg Arg Met Thr Leu Arg Asp Asp Gln Pro Ala Lys
305                 310                 315                 320
Leu Glu Lys Glu Pro Lys Thr Arg Pro Glu Glu Asn Lys Pro Glu Arg
                325                 330                 335
Pro Ser Gly Arg Lys Pro Arg Pro Met Gly Ile Ile Ala Ala Asn Val
            340                 345                 350
Glu Lys His Tyr Glu Thr Gly Arg Val Ile Gly Asp Gly Asn Phe Ala
        355                 360                 365
Val Val Lys Glu Cys Arg His Arg Glu Thr Arg Gln Ala Tyr Ala Met
    370                 375                 380
Lys Ile Ile Asp Lys Ser Arg Leu Lys Gly Lys Glu Asp Met Val Asp
385                 390                 395                 400
Ser Glu Ile Leu Ile Ile Gln Ser Leu Ser His Pro Asn Ile Val Lys
                405                 410                 415
Leu His Glu Val Tyr Glu Thr Asp Met Glu Ile Tyr Leu Ile Leu Glu
            420                 425                 430
Tyr Val Gln Gly Gly Asp Leu Phe Asp Ala Ile Ile Glu Ser Val Lys
        435                 440                 445
Phe Pro Glu Pro Asp Ala Ala Leu Met Ile Met Asp Leu Cys Lys Ala
    450                 455                 460
Leu Val His Met His Asp Lys Ser Ile Val His Arg Asp Leu Lys Pro
465                 470                 475                 480
Glu Asn Leu Leu Val Gln Arg Asn Glu Asp Lys Ser Thr Thr Leu Lys
                485                 490                 495
Leu Ala Asp Phe Gly Leu Ala Lys His Val Val Arg Pro Ile Phe Thr
            500                 505                 510
Val Cys Gly Thr Pro Thr Tyr Val Ala Pro Glu Ile Leu Ser Glu Lys
        515                 520                 525
Gly Tyr Gly Leu Glu Val Asp Met Trp Ala Ala Gly Val Ile Leu Tyr
    530                 535                 540
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Ile Leu Leu Cys Gly Phe Pro Pro Phe Arg Ser Pro Glu Arg Asp Gln
545                 550                 555                 560
Asp Glu Leu Phe Asn Ile Ile Gln Leu Gly His Phe Glu Phe Leu Pro
                565                 570                 575
Pro Tyr Trp Asp Asn Ile Ser Asp Ala Ala Lys Asp Leu Val Ser Arg
            580                 585                 590
Leu Leu Val Val Asp Pro Lys Lys Arg Tyr Thr Ala His Gln Val Leu
        595                 600                 605
Gln His Pro Trp Ile Glu Thr Ala Gly Lys Thr Asn Thr Val Lys Arg
    610                 615                 620
Gln Lys Gln Val Ser Pro Ser Ser Glu Gly His Phe Arg Ser Gln His
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<210> 6
<211> 1947
<212> DNA
<213> Human

<400> 6

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<210> 7

<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence involved in ATP binding

<221> VARIANT
<222> 1
<223> The L at position 1 can be I or V.

<221> VARIANT
<222> 3
<223> The amino acid at position 3 can be any amino acid except P

<221> VARIANT
<222> 5
<223> The amino acid at position 3 can be any amino acid except P

<221> VARIANT
<222> 6
<223> The F at position 6 can be Y, W, M,G, S, T, N, or H

<221> VARIANT
<222> 7
<223> The S at position 7 can be G or A

<221> VARIANT
<222> (8)...(0)
<223> The amino acid at position 8 can be any amino acid except P or W.

<221> VARIANT
<222> (9)...(0)
<223> The L at position 9 can be I, V, C, A, or T.

<221> VARIANT
<222> (10)...(0)
<223> The amino acid at position 10 can be any amino acid except P or D.

<221> VARIANT
<222> (11)...(0)
<223> The amino acid at position 11 can be any amino acid.

<221> VARIANT
<222> (12)...(0)

<223> The G at position 12 can be S, T, A, C, L, I, V, M, F, or Y.

<221> VARIANT
<222> (13)...(0)
<223> The amino acid at position 13 is as few as 5, up to 18, amino acids, and the amino acid can be any amino acid.

<221> VARIANT
<222> (14)...(0)
<223> The L at position 14 can be I, V, M, F, Y, W, C, S, T, A, or R.

<221> VARIANT
<222> (15)...(0)
<223> The A at position 15 can be I, V, or P.

<221> VARIANT
<222> (16)...(0)
<223> The L at position 16 can beI, V, I, M, F, A, G, C, K, or R.

<400> 7
Leu Gly Xaa Gly Xaa Phe Ser Xaa Leu Xaa Xaa Gly Xaa Leu Ala Leu
1 5 10 15
Lys

<210> 8
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Sequence for Serine/Threonine Kinase

<221> VARIANT
<222> 1
<223> The L at position 1 can be I, V, M, F, or Y.

<221> VARIANT
<222> 2
<223> The amino acid at position 2 can be any amino acid.

<221> VARIANT
<222> 3
<223> The H at position 3 can be Y.

<221> VARIANT
<222> 4

<223> The amino acid at position 4 can be any amino acid.

<221> VARIANT
<222> 5
<223> The D at position 5 is an active site residue.

<221> VARIANT
<222> (6)...(0)
<223> The L at position 6 can be I, V, M, F, Y.

<221> VARIANT
<222> (8)...(0)
<223> The amino acid at position 8 is two amino acids, and can be any amino acid.

<221> VARIANT
<222> (10)...(0)
<223> The L at position 10 can be any 3 of L, I, V, M, F, Y, C, T.

<400> 8
Leu Xaa His Xaa Asp Leu Lys Xaa Asn Leu
1 5 10

<210> 9
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Sequence for Tyrosine Kinase

<221> VARIANT
<222> 1
<223> The L at position 1 can be I, V, M, F, Y, or C.

<221> VARIANT
<222> 2
<223> The amino acid at position 2 can be any amino acid.

<221> VARIANT
<222> 3
<223> The H at position 3 can be Y.

<221> VARIANT
<222> 4
<223> The amino acid at position 4 can be any amino acid.

<221> VARIANT
<222> 5
<223> The D at position 5 is an active site residue.

<221> VARIANT
<222> (6)...(0)
<223> The L at position 6 can be I, V, M, F, or Y.

<221> VARIANT
<222> (7)...(0)
<223> The R at position 7 can be S, T, A, or C.

<221> VARIANT
<222> (8)...(0)
<223> The amino acid at position 8 is 2 amino acids, and can be any amino acid.

<221> VARIANT
<222> (10)...(0)
<223> The L at position 10 can be any 3 of L, I, V, M, F, Y, or C.

<400> 9
Leu Xaa His Xaa Asp Leu Arg Xaa Asn Leu
 1   5   10

<210> 10
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Sequence for Tyrosine Kinase Phosphorylation Site

<221> VARIANT
<222> 1
<223> The R at position 1 can be K.

<221> VARIANT
<222> 2
<223> The amino acid at position 2 can be two or three amino acids, and the amino acid can be any amino acid.

<221> VARIANT
<222> (3)...(0)
<223> The D at position 3 can be E.

<221> VARIANT
<222> 4
<223> The amino acid at position 2 can be two or three amino acids, and the amino acid can be any amino acid.